

FULL LISTING OF THE CURRENT PENDING CLAIMS

1. **(Currently amended)** A method for identifying previously unidentified in diet-regulated disease-associated polynucleotides comprising the steps of:

(i) selecting a cohort from each of at least two different inbred rodent ~~known mammalian~~ genotypes (A and B) all of the same generation and all either male or virgin female, one of these genotypes (A) being susceptible to a disease, and the other genotype (B) not susceptible to the same disease;

(ii) dividing each genotype cohort into two groups (A1 and A2 and B1 and B2);

(iii) for each genotype cohort, each group is fed a different diet (A1 is fed diet No.1 and A2 is fed diet No.2, and similarly for B1 and B2);

(iv) measuring gene expression and comparing expression across the strains individuals that differ in either genotype or in diet, but not in both;

(v) analyzing the expression data so as to identify diet-regulated disease-associated genes in the disease-susceptible strain one or more genes that shows at least a two-fold increase or decrease in gene expression;

(vi) matching the genes shown above to have at least a two-fold increase or decrease in gene expression with one or more independently-derived quantitative trait loci (QTLs) known to encode one or more genes that contribute to the development of a disease,

(vii) wherein the genes so identified are considered to be a diet-regulated disease-associated genes.

2-3. **(Cancelled)**

4. **(Currently amended)** The method of claim [[2]] 1 wherein gene expression is compared by comparing mRNA abundance.

5-16. **(Cancelled)**

17. (New) The method of claims 1 wherein gene expression is compared across individuals that differ in genotype only.

18. (New) The method of claim 1 wherein gene expression is compared across individuals that differ in diet only.

20. (New) The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to encode one or more genes that contribute to diabetes.

21. (New) The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to encode one or more genes that contribute to obesity.

22. (New) The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to encode one or more genes that contribute to Alzheimer's disease.

23. (New) The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to encode one or more genes that contribute to a cardiovascular disease.

24. (New) The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to encode one or more genes that contribute to cancer.

25. (New) The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to encode one or more genes that contribute to hypertension.